

BEST AVAILABLE COPY

US-08-943-776-1.rng

Fri Jul 17 07:49:29 1998

/note= "Max-interacting protein-2"

FT W09417101-A.
 PN 04-AUG-1994.
 PD 29-DEC-1993; U12643.
 PF 29-JAN-1993; US-011398.
 PR (GEO) GEN HOSPITAL-CORP.
 PA Brent R, Zervos AS;
 PI WPI: 94-264033/32.
 DR P-PSDB; R56543.
 DT Max-interacting polypeptide and DNA encoding them - used as
 PT anticancer agents and to screen for agents which inhibit cellular
 PT proliferation
 PT Disclosure: Page 41; 57pp; English.
 PS The DNA encodes Max-interacting (Mxi) protein-2. Detection of Mxi
 CC gene expression can be used to detect malignant cells in biological
 CC samples. The Mxi protein-2 and sense/antisense RNA can be delivered
 CC to e.g. bone marrow as therapeutic agents for cancer. 299 T;
 CC Sequence 1200 BP; 306 A; 270 C; 325 G; 299 T;
 SQ

Query Match 4.1%; Score 75; DB 12; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 1.73e-24;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 actcactataggcggaattgggtaccggccccccctcgaggtcgaggtatcgataagc 76
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 Cp 1847 ACTCATTATAGGGGAATTGGGTACCGGGCCCCCTCGAGGTGCGAGGTATCGATAAGC 1788

Db 77 ttgatatcgaaattcc 91
 |||||||
 Cp 1787 TTGATATCGAATTCC 1773

RESULT 8 CDNA to mRNA; 2150 BP.

ID T91037; standard; CDNA to mRNA; 2150 BP.
 AC T91037;
 DT 25-FEB-1998 (first entry)
 DE Yeast checkpoint control gene RAD17 CDNA.
 KW RAD17; cell cycle; checkpoint gene; yeast; DNA damage;
 KW cancer; therapy; ss.
 OS Saccharomyces cerevisiae.
 FH Key Location/Qualifiers
 FT Key 741..1946
 FT CDS /*tag= a
 FT
 PN US5674996-A.
 PD 07-OCT-1997.
 PF 12-MAY-1992; 882051.
 PR 18-FEB-1994; US-198446.
 PR 12-MAY-1992; US-882051.
 PR 14-MAY-1992; US-884426.
 PR 12-MAY-1993; WO-U04458.
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 PA (UNIV) UNIV ARIZONA.
 PA (UNIW) UNIV WASHINGTON.
 PN Groudine MT, Hartwell LH, Pion SE, Weinert TA;
 PI WPI: 97-502392/46.
 DR P-PSDB; W26661.
 DT Nucleotide sequence capable of hybridising with huCDC34 - which is
 PT human checkpoint gene, useful to increase sensitivity of tumour
 PT cells to chemotherapeutic drugs or radiation
 PT Example 4; Column 41-46; 54pp; English.
 PS Novel yeast checkpoint control genes RAD17, RAD24, MEC1, MEC2 and
 CC MEC3 (see T91037-41, respectively) are responsible for recognising
 CC if the cell has suffered DNA damage in the form of radiation or
 CC chemical damage or if the cell has failed to complete DNA
 CC replication because of chemical inhibition or intrinsic error.
 CC Upon recognising damage or failure, the genes are responsible
 CC for inhibiting mitosis. The purpose of this checkpoint control
 CC is that it preserves the viability of the cell and the integrity
 CC of the genome by providing the cell time to repair these insults
 CC prior to undertaking mitosis. The genes are potentially useful in
 CC developing cancer chemotherapeutics, cancer chemoprevention
 CC agents and environmental toxicology tests. They can be used to
 CC screen for

CC chemical agents that would interfere with checkpoint controls.
 CC Cloned genes can also be used to develop yeast strains in which to
 CC these genes are deleted. Such yeast strains can then be used to
 CC find the homologous human genes (see T91034-36).
 CC Sequence 2150 BP; 748 A; 372 C; 425 G; 605 T;
 SQ

Query Match 4.1%; Score 75; DB 35; Length 2150;
 Best Local Similarity 100.0%; Pred. No. 1.73e-24;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Cp 1847 ACTCATTATAGGGGAATTGGGTACCGGGCCCCCTCGAGGTGCGAGGTATCGATAAGC 1788

Db 129 ttgatatcgaaattcc 143
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 Cp 1787 TTGATATCGAATTCC 1773

RESULT 9 DNA; 3792 BP.

ID Q48463;
 AC Q48463;
 DT 18-MAR-1994 (first entry)
 DE Plasmid pG+host4 containing Ts replication system.
 DE Temperature sensitive replication; antibiotic resistance marker gene;
 KW site-specific recombination; chromosomal integration; inactivation;
 KW heterologous gene expression; thermosensitive plasmid; ds.
 OS Synthetic.
 PN WO9318164-A.
 PD 16-SEP-1993.
 PF 12-MAR-1993; F00248.
 PR 13-MAR-1992; FR-003034.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PI Gruss A, Maguin E;
 PI WPI: 93-303478/38.
 DR New bacterial plasmid contg. heat sensitive replication system -
 PT and marker gene, opt. capable of chromosomal integration, used to
 PT inactivate specific gene or introduce heterologous gene
 PT Example 2; Fig 9; 73pp; French.
 PS Plasmid pGK12 (Appl. Environ. Microbiol., 48; 726 (1984)) contg. two
 CC antibiotic resistance marker genes was subjected to mutagenesis with
 CC hydroxylamine. A heat-stable mutant was isolated (coding for a heat-
 CC sensitive RepA - see Q48466 and Q48467), cut with ClaI and HpaII and
 CC the 340bp fragment lacking the Cm resistance gene was ligated to a
 CC 445bp PvuII fragment of pBluescript SK+ containing a multicloning
 CC site, T7 and T3 promoters and sequencing primer binding sites. The
 CC resulting plasmid was designated pVE5004 (or pG+host4 - Q48463). It
 CC is thermosensitive in all hosts tested, including E.coli, and must be
 CC maintained at 28 deg.C.
 SQ Sequence 3792 BP; 1249 A; 552 C; 742 G; 1249 T;

Query Match 4.1%; Score 75; DB 8; Length 3792;
 Best Local Similarity 100.0%; Pred. No. 1.73e-24;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3448 actcactataggcggaattgggtaccggccccccctcgaggtcgaggtatcgataagc 3507
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Db 3508 ttgatatcgaaattcc 3522
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 Cp 1787 TTGATATCGAATTCC 1773

RESULT 10 DNA; 5234 BP.

ID Q48464;
 AC Q48464;
 DT 18-MAR-1994 (first entry)
 DE Plasmid pG+host5 containing Ts replication system.
 DE Temperature sensitive replication; antibiotic resistance marker gene;
 KW site-specific recombination; chromosomal integration; inactivation;
 KW heterologous gene expression; thermosensitive plasmid; ds.
 OS Synthetic.

1

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: April 19, 2001, 15:26:43 ; Search time 50.46 Seconds
(without alignments)
148.397 Million cell updates/sec

Title: US-08-943-776-2
Perfect score: 2323
Sequence: 1 MEQPRGCAVAAALLVLL.....ERMGLDGVCLRLRQRP 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgnl_7/ptodata/1/iaa/PTCUS.COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2267	97.6	428	3	US-08-815-469-2
3	376	16.2	455	1	US-08-050-319B-25
4	376	16.2	455	2	US-08-465-982-25
5	374	16.1	455	1	US-08-321-668-2
6	374	16.1	455	1	US-08-837-941-2
7	374	16.1	455	2	US-08-126-016-2
8	374	16.1	455	3	US-08-815-469-5
9	217	9.3	280	3	US-08-974-022-46
10	210	9.0	199	1	US-08-050-319B-48
11	210	9.0	199	2	US-08-465-982-48
12	207.5	8.9	283	4	PCT-US96-12374-2
13	203.5	8.8	440	3	US-08-883-036A-2
14	200.5	8.6	153	2	US-08-219-237B-4
15	199.5	8.6	335	2	US-08-219-237B-2
16	199.5	8.6	335	2	US-08-409-338-1
17	199.5	8.6	335	4	PCT-US95-17083-2
18	198.5	8.5	154	2	US-08-232-087A-10
19	197.5	8.5	335	3	US-08-815-469-6
20	189.5	8.2	368	2	US-08-651-579-2
21	176.5	7.6	219	3	US-08-974-022-45
22	175.5	7.6	158	1	US-08-050-319B-54
23	175.5	7.6	158	2	US-08-465-982-54
24	168	7.2	314	1	US-08-444-231-19
25	168	7.2	314	1	US-08-152-443A-19
26	168	7.2	314	4	PCT-US95-17083-4
27	166	7.1	167	1	US-08-050-319B-2
28	166	7.1	167	1	US-08-050-319B-57

Sequence 2, Appl1
Sequence 57, Appl1
Sequence 4, Appl1
Sequence 6, Appl1
Sequence 6, Appl1
Sequence 15, Appl1
Sequence 3, Appl1
Sequence 11, Appl1
Sequence 11, Appl1
Sequence 4, Appl1
Sequence 6, Appl1
Sequence 50, Appl1
Sequence 50, Appl1
Sequence 2, Appl1
Sequence 20, Appl1
Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-815-469-4
Sequence 4, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-815-469-4

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NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-815-469-2

Query Match	97.6%	Score 2267;	DB 3;	Length 428;
Best Local Similarity	97.1%;	Pred. No. 7.5e-189;		
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QY	57	LKAPCTPCGNGSTCLV	CGPQDTFLAWENHNHSECA	RCACDEQASOVALENCSAVADTRCG 116
Db	68	LKAPCTPCGNGSTCLV	CGPQDTFLAWENHNHSECA	RCACDEQASOVALENCSAVADTRCG 127
QY	117	CKPGWFVECVQSCV	SSSPYQCPLDCGALHRRH	LLCRRDTCGTCPLPGFVEHGDGC 176
Db	128	CKPGWFVECVQSCV	SSSPYQCPLDCGALHRRH	LLCRRDTCGTCPLPGFVEHGDGC 187
QY	177	VSCPTSLGSCPERCA	AVCGWRMFVVOLLAGLV	PLLLGATLTYTRCWFHPKLVTVA 236
Db	188	VSCPTSLGSCPERCA	AVCGWRMFVVOLLAGLV	PLLLGATLTYTRCWFHPKLVTVA 247
QY	237	DEAGMEALTPPPATH	LSPLDSATLLIAPDSS	SEKICTVLQVGNSTPGYPETEALCPQV 296
Db	248	DEAGMEALTPPPATH	LSPLDSATLLIAPDSS	SEKICTVLQVGNSTPGYPETEALCPQV 307
QY	297	TWSWDQLPSRALG	PAAAPTLSPESPAGSPAM	LOPGPOLYDVMADVPARRWKEFVFTLGL 356
Db	308	TWSWDQLPSRALG	PAAAPTLSPESPAGSPAM	LOPGPOLYDVMADVPARRWKEFVFTLGL 367
QY	357	REAEIEAVEIGEIR	FRDQOYEMLKRWQQOQ	PAGLGAVYAALERMGLDGCVEDLRSRLQRG 416
Db	368	REAEIEAVEIGEIR	FRDQOYEMLKRWQQOQ	PAGLGAVYAALERMGLDGCVEDLRSRLQRG 427
QY	417	P	417	
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RESULT 2
US-0 -815469-2
Sequence 2, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
PENDING AGENT INFORMATION:

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 10:49:23 ; Search time 65.08 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	75.4	4.1	1200	1	US-08-011-398B-3
7	75.4	4.1	1200	1	US-08-464-051-3
8	75.4	4.1	1200	2	US-08-462-498-3
9	75.4	4.1	2150	1	US-08-198-446B-10
10	75.4	4.1	2150	2	US-08-870-693-10
11	75.4	4.1	3792	2	US-08-992-334-1
12	75.4	4.1	3792	3	US-08-302-752-1
13	75.4	4.1	5234	2	US-08-992-334-2
14	75.4	4.1	6722	3	US-08-302-752-2
15	75.4	4.1	6722	2	US-08-992-334-3
16	75.4	4.1	6722	3	US-08-302-752-3
17	74.4	4.0	2605	2	US-08-680-395-4
18	74.2	4.0	5534	1	US-08-452-267-3
19	74.2	4.0	5534	3	US-09-123-644-3
20	70.6	3.8	2161	3	US-09-106-038A-1
21	70.6	3.8	2175	1	US-08-321-668-1
22	70.6	3.8	2175	1	US-08-837-941-1
23	70.6	3.8	2175	1	US-08-126-016-1
24	69	3.7	2062	1	US-08-050-319B-24
25	69	3.7	2062	2	US-08-463-982-24
26	68.8	3.7	685	1	US-08-463-115-56
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29	67	3.6	4525	2	US-08-613-861-2	Sequence 2, Appli
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31	65	3.5	4965	3	US-08-675-566-22	Sequence 22, Appli
32	62	3.4	6994	3	US-08-675-566-1	Sequence 1, Appli
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36	59	3.2	834	2	US-08-967-101-113	Sequence 113, App
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ALIGNMENTS

RESULT 1
US-08-815-469-1
; Sequence 1, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: CDNA

[illegible]

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661	Db	ACCTACACATACCGCCACTGTCGCCCTCAAGGCCCTGGTTACTGCAGATGAAGCTGGG	720
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721	Db	ATGGAGGCTCTGACCCACACACCGCCACCATCTGTCACCTTGGACACGCGCCACACC	780
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781	Db	CTTCTAGCACTCTCTGACAGCAGTGAAGAATCTGCACCGTCCAGTTGGTGGGTAAACAGC	840
1076	QY	TGGACCCCTGGCTACCCCGAGACCCAGGAGCGCTCTGCCCGCAGGTGACATGGTCTCTGG	1135
841	Db	TGGACCCCTGGCTACCCCGAGACCCAGGAGCGCTCTGCCCGCAGGTGACATGGTCTCTGG	900
1136	QY	GACCAGTTGCCGACGAGCTCTTGGGCCCCGCTGCTGGGCCACACATCTGCCGAGAGTCC	1195
901	Db	GACCAGTTGCCGACGAGCTCTTGGGCCCCGCTGCTGGGCCACACATCTGCCGAGAGTCC	960
1196	QY	CGAGCGGGCTGCCAGCCATGATGCTGCAGCGCGGGCCCCGAGCTCTACGAGCTGATGGAC	1255
961	Db	CGAGCGGGCTGCCAGCCATGATGCTGCAGCGGGCCCCGAGCTCTACGAGCTGATGGAC	1020
1256	QY	GCGGTCCCAGCGCGGCTGGAAGAGTTCGTGGCGACGCTGGGGCTCGCGAGGCGAGAG	1315
1021	Db	GCGGTCCCAGCGCGGCTGGAAGAGTTCGTGGCGACGCTGGGGCTCGCGAGGCGAGAG	1080
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1376	QY	CGTGTGCGCCAGCAGACGCCCGGGCCCTCGGAGCCGTTTACGGGCCCCCTGGAGCGCATG	1435
1141	Db	CGTGTGCGCCAGCAGACGCCCGGGCCCTCGGAGCCGTTTACGGGCCCCCTGGAGCGCATG	1200
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